

Glycomics, a focus of the postgenomic era

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A major lesson from eukaryotic genome sequencing projects is that the absolute number of genes an organism's genome encodes is not the best parameter for defining complexity of function. It appears that the complex functions associated with human health and disease are determined by combinatorial expansion of genomic information in the form of posttranslational modifications. Of these, the most complex and ubiquitous is glycosylation, highlighting the importance of glycobiology in the postgenomic era. This presentation will focus on new chemical approaches for profiling glycosylation at the systems level in both cells and living animals.